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AGTTCCCATCTCAGAAGGCTCAATGAAATCCTTCCTTCCTGTCCACACCATCGTGCTTATCAGGGAGAATGTGTGCAAG
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AGGAATTTCCTACCGACGCCTTTGGGGATATTCAGTTTGAGACACTGGGGAAGAAAGGGAAGTATATACGTCTGTCCTG
CGACACGGACGCGGAAATCCTTTACGAGCTGCTGACCCAGCACTGGCACCTGAAAACACCCAACCTGGTCATTTCTGTG
ACCGGGGGCGCCAAGAACTTCGCCCTGAAGCCGCGCATGCGCAAGATCTTCAGCCGGCTCATCTACATCGCGCAGTCCA
AAGGTGCTTGGATTCTCACGGGAGGCACCCATTATGGCCTGATGAAGTACATCGGGGAGGTGGTGAGAGATAACACCAT
CAGCAGGAGTTCAGAGGAGAATATTGTGGCCATTGGCATAGCAGCTTGGGGCATGGTCTCCAACCGGGCACCCTCATC
AGGAATTGCGATGCTGAGGGCTATTTTTTAGCCCAGTACCTTATGGATGACTTCACAAGAGATCCACTGTATATCCTGG
ACAACAACCACACACATTTGCTGCTCGTGGACAATGGCTGTCATGGACATCCCACTGTCGAAGCAAAGCTCCGGAATCA
GCTAGAGAAGTATATCTCTGAGCGCACTATTCAAGATTCCAACTATGGTGGCAAGATCCCCATTGTGTGTTTTGCCCAA
GGAGGTGGAAAAGAGACTTTGAAAGCCATCAATACCTCCATCAAAAATAAAATTCCTTGTGTGGTGGTGGAAGGCTCGG
GCCAGATCGCTGATGTGATCGCTAGCCTGGTGGAGGTGGAGGATGCCCTGACATCTTCTGCCGTCAAGGAGAAGCTGGT
GCGCTTTTTACCCCGCACGGTGTCCCGGCTGCCTGAGGAGGAGACTGAGAGTTGGATCAAATGGCTCAAAGAAATTCTC
GAATGTTCTCACCTATTAACAGTTATTAAAAATGGAAGAAGCTGGGGATGAAATTGTGAGCAATGCCATCTCCTACGCTC
TATACAAAGCCTTCAGCACCAGTGAGCAAGACAAGGATAACTGGAATGGGCAGCTGAAGCTTCTGCTGGAGTGGAACCA
GCTGGACTTAGCCAATGATGAGATTTTCACCAATGACCGCCGATGGGAGAAGAGCAAACCGAGGCTCAGAGACACAATA
ATCCAGGTCACATGGCTGGAAAATGGTAGAATCAAGGTTGAGAGCAAAGATGTGACTGACGGCAAAGCCTCTTCTCATA
TGCTGGTGGTTCTCAAGTCTGCTGACCTTCAAGAAGTCATGTTTACGGCTCTCATAAAGGACAGACCCAAGTTTGTCCG
CCTCTTTCTGGAGAATGGCTTGAACCTACGGAAGTTTCTCACCCATGATGTCCTCACTGAACTCTTCTCCAACCACTTC
AGCACGCTTGTGTACCGGAATCTGCAGATCGCCAAGAATTCCTATAATGATGCCCTCCTCACGTTTGTCTGGAAACTGG
TTGCGAACTTCCGAAGAGGCTTCCGGAAGGAAGACAGAAATGGCCGGGACGAGATGGACATAGAACTCCACGACGTGTC
TCCTATTACTCGGCACCCCCTGCAAGCTCTCTTCATCTGGGCCATTCTTCAGAATAAGAAGGAACTCTCCAAAGTCATT
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CAGCAGCGATGAAGACTTGGCAGAACAGCTGCTGGTCTATTCCTGTGAAGCTTGGGGTGGAAGCAACTGTCTGGAGCTG
GCGGTGGAGGCCACAGACCAGCATTTCATCGCCCAGCCTGGGGGTCCAGGAGGGGAGGGCTGTGCCCGTCCCATGCTTGC
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TGGCGTTCTTCACCTCCCCCTTCGTGGTCTTCTCCTGGAATGTGGTCTTCTACATCGCCTTCCTCCTGCTGTTTGCCTA
CGTGCTGCTCATGGATTTCCATTCGGTGCCACACCCCCCCGAGCTGGTCCTGTACTCGCTGGTCTTTGTCCTCTTCTGT
GATGAAGTGAGACAGATGGAGCAGGGGGTGGCGCTCGTGGAGGAGGCTCGGGCAGCACAGGAGCCCACTGAGGGGGTGG
GAGGCTCAGGCATGGTGGGCTGCAGGTCCCGAGCCCTGCCCCACGGGAAGGCAGCTACGGCCCGCCCCGGTTCCCGCTC
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TGCAGCGGTGGGCTGAAGGGCTCCTCAAGTGCCGCCAAAGTGGGAGCCCAGGCAGAGGAGGTGCCGAGAGCAAGCGAGG
GCTGTGAGGACTGCCAGCACGCTGTCACCTCTCAGAAGCGTAAGGGACTGGCTGATGTCTTATCACGGACTGGGAACAA
CTGGGACAGTGTCTGCCCCACAAGTGGGTGGTACGTAAATGGGGTGAATTATTTTACTGACCTGTGGAATGTGATGGAC
ACGCTGGGGCTTTTTTACTTCATAGCAGGAATTGTATTTCGGCTCCACTCTTCTAATAAAAGCTCTTTGTATTCTGGAC
GAGTCATTTTCTGTCTGGACTACATTATTTTCACTCTAAGATTGATCCACATTTTTTACTGTAAGCAGAAACTTAGGACC
CAAGATTATAATGCTGCAGAGGATGACGAGCATTGAGATGAGCTCATCTGGAAGCTCCATTCCAACACTGAGGTTCTTT
GAGTTTGTGGTTTTAATTCAAAGCATTTCTGGGACATCCAGTCATCATGAAGTCATGCTATCTGATCGATGTGTTCTTC
TTCCTGTTCCTCTTTGCGGTGTGGATGGTGGCCTTTGCGTGGCCAGGCAAGGGATCCTTAGGCAGAATGAGCAGCGCTG
GAGGTGGATATTCCGTTCGGTCATCTACGAGCCCTACCTGGCCATGTTCGGCCAGGTGCCCAGTGACGTGGATGGTACC
ACGTATGACTTTGCCCACTGCACCTTCACTGGGAATGAGTCCAAGCCACTGTGTGTGGAGCTGGATGAGCACAACCTGC
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GGTCGCCATGTTTGGGTGTGTAGCCGGTGGGCTAGTTCAGGTTCTTGACTTTGGGACAGAAAATAATTTGAAAGTGAGT
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CAGCTGTCACTGCATGTCTCCAGCCAGCTAGGTGTTTGCCAGGGACAGGACGCCAAGGGCACAAGATATCGCTGGAGAT
GCACAAAGGGAAAATTGCAGAATTCTCTCAGGGACAACACCAGATGGCCACTGGTTGTCAAGGAGACTTTAAGAACCAT
CTCAGATGGGGCGGCTACACGGTGGGCACCGTCCAGGAGAACAATGACCAGGTCTGGAAGTTCCAGAGGTACTTCCTGG
TGCAGGAGTACTGCAGCCGCCTCAATATCCCCTTCCCCTTCATCGTCTTCGCTTACTTCTACATGGTGGTGAAGAAGTG
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GTTGCCTGTTTTATTTGGAGGGCATTGGAAATGCGTGA

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MASWCLITAQ VWVKMKGDVV GSRSPQQHKR STGTPQGLPV PISEGSMKSF LPVHTIVLIR
ENVCKCGYAQ SQHMEGTQIN QSEKWNYKKH TKEFPTDAFG DIQFETLGKK GKYIRLSCDT
DAEILYELLT QHWHLKTPNL VISVTGGAKN FALKPRMRKI FSRLIYIAQS KGAWILTGGT
HYGLMKYIGE VVRDNTISRS SEENIVAIGI AAWGMVSNRD TLIRNCDAEG YFLAQYLMDD
FTRDPLYILD NNHTHLLLVD NGCHGHPTVE AKLRNQLEKY ISERTIQDSN YGGKIPIVCF
AQGGGKETLK AINTSIKNKI PCVVVEGSGQ IADVIASLVE VEDALTSSAV KEKLVRFLPR
TVSRLPEEET ESWIKWLKEI LECSHLLTVI KMEEAGDEIV SNAISYALYK AFSTSEQDKD
NWNGQLKLLL EWNQLDLAND EIFTNDRRWE KSKPRLRDTI IQVTWLENGR IKVESKDVTD
GKASSHMLVV LKSADLQEVM FTALIKDRPK FVRLFLENGL NLRKFLTHDV LTELFSNHFS
TLVYRNLQIA KNSYNDALLT FVWKLVANFR RGFRKEDRNG RDEMDIELHD VSPITRHPLQ
ALFIWAILQN KKELSKVIWE QTRGCTLAAL GASKLLKTLA KVKNDINAAG ESEELANEYE
TRAVELFTEC YSSDEDLAEQ LLVYSCEAWG GSNCLELAVE ATDQHFIAQP GVQRGGLCPS
HACKDADDAL ISGSRKKPVD KHKKLLWYYV AFFTSPFVVF SWNVVFYIAF LLLFAYVLLM
DFHSVPHPPE LVLYSLVFVL FCDEVRQMEQ GVALVEEARA AQEPTEGVGG SGMVGCRSRA
LPHGKAATAR PGSRSRHSFH TSLQAEGASS GLGQPRKGLP QCSGGLKGSS SAAKVGAQAE
EVPRASEGCE DCQHAVTSQK RKGLADVLSR TGNNWDSVCP TSGWYVNGVN YFTDLWNVMD
TLGLFYFIAG IVFRLHSSNK SSLYSGRVIF CLDYIIFTLR LIHIFTVSRN LGPKIIMLQR
MTSIEMSSSG SSIPTLRFFE FVVLIQSISG TSSHHEVMLS DRCVLLPVPL CGVDGGLCVA
RQGILRQNEQ RWRWIFRSVI YEPYLAMFGQ VPSDVDGTTY DFAHCTFTGN ESKPLCVELD
EHNLPRFPEW ITIPLVCIYM LSTNILLVNL LVAMFGCVAG GLVQVLDFGT ENNLKVSQKQ
KQARELTAKP KYTLAAAGFR RWTSAVTACL QPARCLPGTG RQGHKISLEM HKGKIAEFSQ
GQHQMATGCQ GDFKNHLRWG GYTVGTVQEN NDQVWKFQRY FLVQEYCSRL NIPFPFIVFA
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IRCLFYLEGI GNA
```
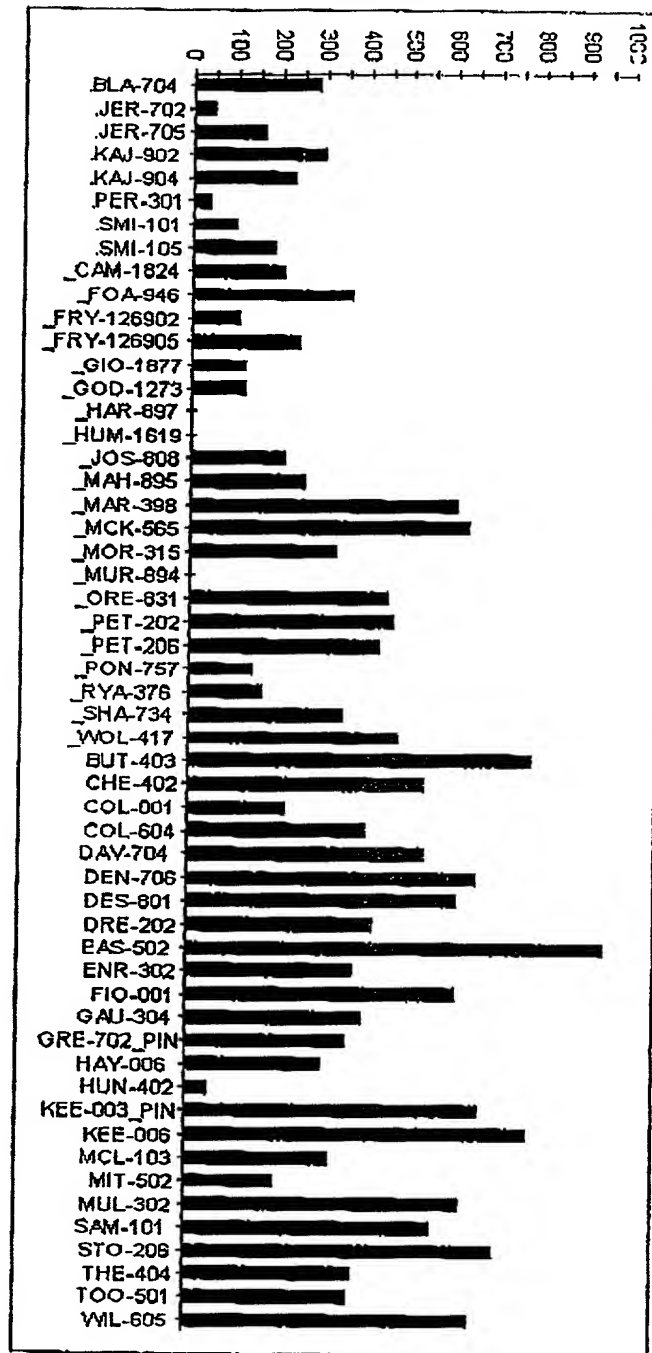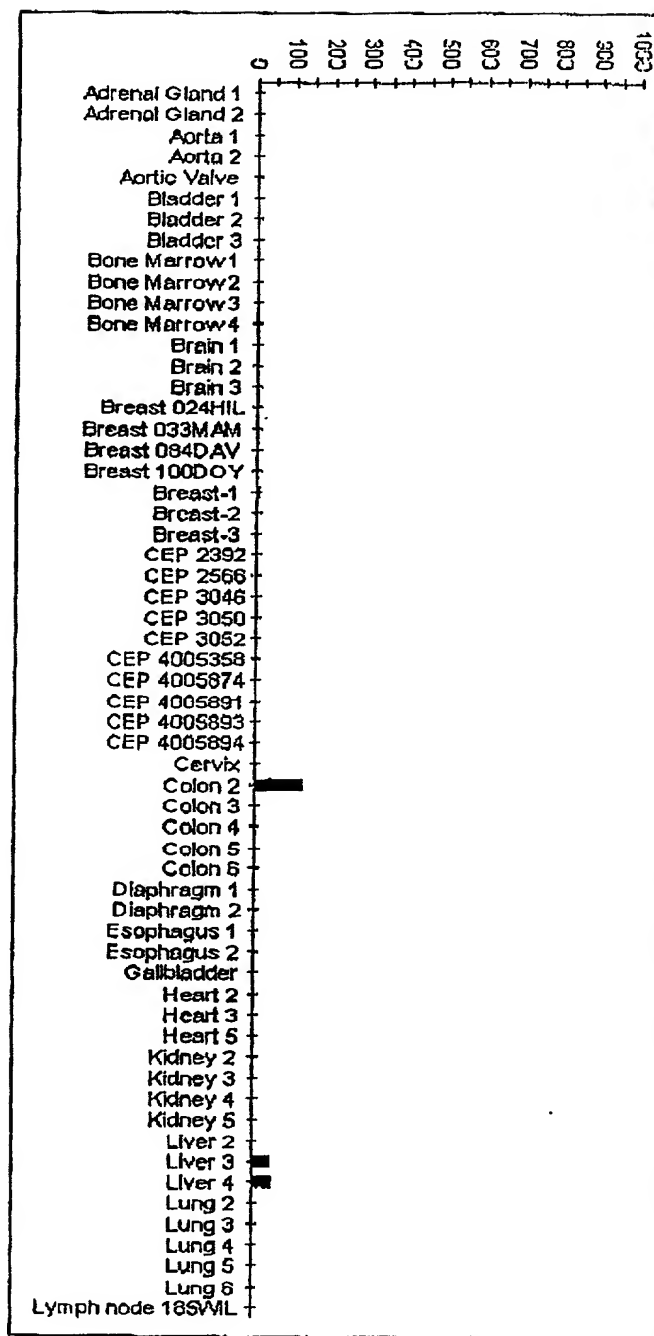
FIGURE 2

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FIGURE 3A

FIGURE 3B

FIGURE 3C

Muscle 1
Muscle 2
Muscle 3
Muscle 4
Muscle 5
ovary 1
ovary 2
Pancreas 1
Pancreas 2
Pancreas 3
Pancreas 4
Prostate 2
Prostate 3
Prostate N180
Prostate N182
Rectum
Salivary Gland
Skin 1
Skin 2
Skin 3
Skin 4
Small intestine 1
Small Intestine 2
Small Intestine 3
Small Intestine 4
SMI-ileum 1
SMI-jejunum 1
Spinal Cord
Spleen 2
Spleen 3
Spleen 4
Spleen 5
Stomach 1
Stomach 2
Stomach 3
Stomach 4
Testis 3
Thymus 1
Thymus 2
Thyroid 1
Trachea 1
Trachea 2
Trachea 3
ureter 1
ureter 2
Uterus 1
Uterus 2
Uterus 3
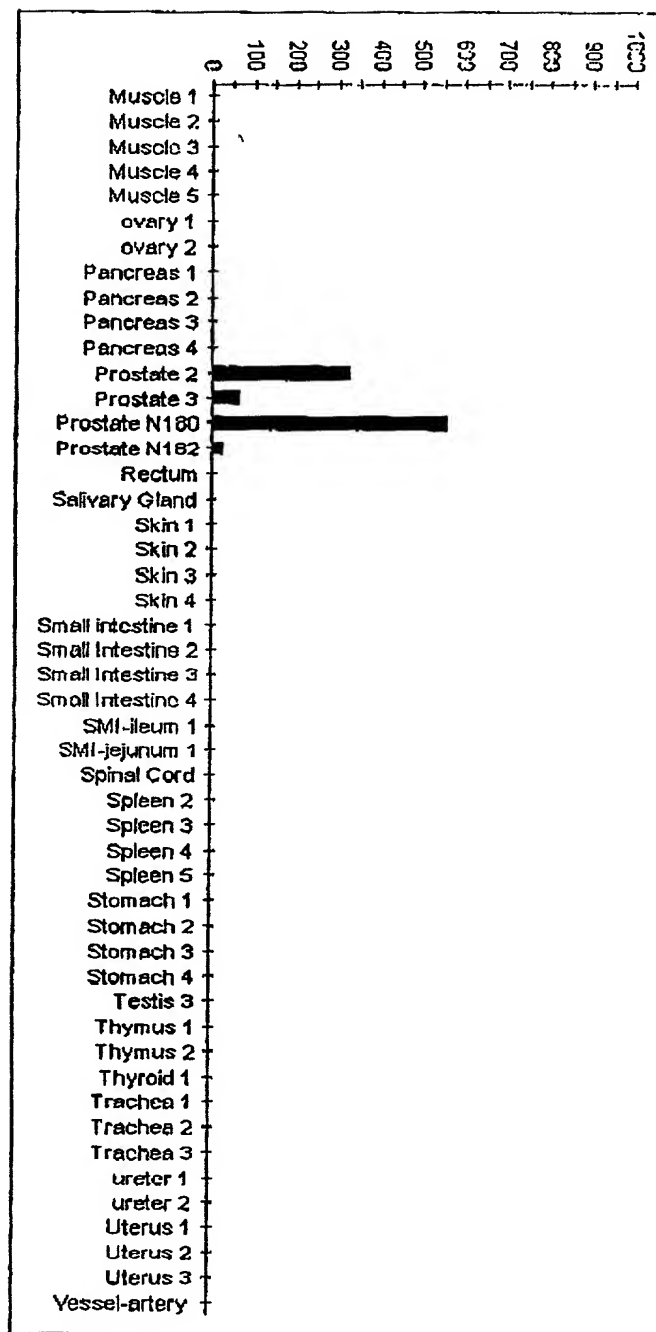Vessel-artery

0 100 200 300 400 500 600 700 800 900 1000

Score = 457 bits (1162), Expect = e-127
Identities = 267/694 (38%), Positives = 385/694 (55%), Gaps = 88/694 (12%)

```
Query:  63  VCKCGYAQSQRMEGT---QINQSEKWNYKKHTKEFPTDAFGDIQFETLGKK-GKYIRLSC 118
            VC+CGY  QH+E       Q  +W+ KKH +E PTDAFGDI F  L +K  KY+R+S
Sbjct:  88  VCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQEMPTDAFGDIVFTGLSQKVKKYVRVSQ 147

Query: 119  DTDAEILYELLTQHWHLKTPNLVISVTGGAKNFALKPRMRKIFSR-LIYIAQSKGAWILT 177
            DT + ++Y L+TQHW L  PNL+ISVTGGAKNF +KPR++ IF R L+ +AQ+ GAWI+T
Sbjct: 148  DTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNFNMKPRLKSIFRRGLVKVAQTTGAWIIT 207

Query: 178  GGTHYGLMKYIGEVVRDNTISRSSEEN-IVAIGIAAWGMVSNRDTLIRNCDAEGYFLAQY 236
            GG+H G+MK +GE VRD ++S S +E  ++ IG+A WG V  R+ LI     G F A+Y
Sbjct: 208  GGSHTGVMKQVGEAVRDFSLSSSYKEGELITIGVATWGTVHRREGLIH---PTGSFPAEY 264

Query: 237  LMDDYTRDFLYILDNNHTHLLLVDNGCHGHPTVEAKLRNQLEKYISERTIQDSNYGGKIP 296
            ++D+  + L LD+NH+H +LVD+G HG  VE  LR +LEK+ISE+T +    KIP
Sbjct: 265  ILDEDGQGNLTCLDSNHSHPILVDDGTHGQYGVEIPLRTRLEKFISEQTKERGGVAIKIP 324

Query: 297  IVCFAQGGGKETLKAINTSIKNKIPCVVVEGSGQIADVIASLVEVE-DALTSSAVKEKLV 355
            IVC   GG  TL  I+ + N PCVVVEGSG++ADVIA + +     +T S +++KL
Sbjct: 325  IVCVVLESGPGTLHTIDNATTNGTPCVVVEGSGRVADVIAQVANLPVSDITISLIQQKLS 384

Query: 356  RFLPRTVSRLPEEETESWIKWLKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFSTS 415
             F        E      W K +++I+   LLTV +  + G + V  AI  AL KA  +
Sbjct: 385  VFFQEMFETFTESRIVEWTKKIQDIVRRQLLTVFREGKDGQQDVDVAILQALLKASRSQ 444

Query: 416  EQ-DKDNWNGQLKLLLEWNQLDLANDEIFTNDRRWEKSKPRLRDTIIQVTWLENGRIKVE 474
            +   +NW+ QLKL + WN++D+A  EIF ++ +W
Sbjct: 445  DHFGHENWDHQLKLAVAWNRVDIARSEIFMDEWQW-------------------------- 479

Query: 475  SKDVTDGKASSHMLVVLKSADLQEVMFTALIKDRPKFVRLFLENGLNLRKFLTHDVLTEL 534
                          K +DL   M  ALI ++P+FV+LFLENG+ L++F+T D L  L
Sbjct: 480  ----------------KPSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYL 522

Query: 535  FSN-HFSTLVYRNLQ--------------IAKNSYNDALLTFVWKLVANFRRGFRKEDRN 579
            + N  S L + LQ              A        + +L+ +F +     R+
Sbjct: 523  YENLDPSCLFHSKLQKVLVEDPERPACAPAAPRLQMHHVAQVLRELLGDFTQPLYPRPRH 582

Query: 580  GR--------DEMDIELHDVS------------PITRHPLQALFIWAILQNKKELSKVIW 619
              + + + VS            T  P++ L IWAI+QN++EL+ +IW
Sbjct: 583  NDRLRLLLPVPHVKLNVQGVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIW 642

Query: 620  EQTRGCTLAALGASKLLKTLAKVKNDINAAGESEELANEYETRAVELFTECYSSDEDLAE 679
             Q++ C  AAL  SK+LK L+K + D +++ E   LA EYE RA+ +FTECY  DE+ A+
Sbjct: 643  AQSQDCIAAALACSKILKELSKEEEDTDSSEEMLALAEEYEHRAIGVFTECYRKDEERAQ 702

Query: 680  QLLVYSCEAWGGSNCLELAVEATDQHFIAQPGVQ 713
            +LL   EAWG +  CL+LA+EA D F++  G+Q
Sbjct: 703  KLLTRVSEAWGKTTCLQLALEAKDMKFVSHGGIQ 736
```

FIGURE 4A

Score = 65.6 bits (157), Expect = 2e-10
Identities = 31/57 (54%), Positives = 40/57 (69%)

Query: 38 APFTSPFVVFSWNVVFYIAFLLLFAYVLLMDFHSVPHPPELVLYSLVFVLFCDEVRQ 94
           AFFT+P VVF N++ Y AFL LFAYVL++DF VP   E +Y +F L C+E+RQ
Sbjct: 790 AFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLNLFSLVCEEMRQ 846

FIGURE 4B

```
Score =  163 bits (409), Expect = 4e-39
Identities = 90/227 (39%), Positives = 129/227 (56%), Gaps = 43/227 (18%)

Query: 144   YFTDLWNVMDTLGLFYFIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLRLIHIFTVSRN 203
             YF+D WN +D     F+AG+  RL  +   +LY GRVI  LD+I+F LRL+HIFT+S+
Sbjct: 863   YFSDFWNKLDVGAILLFVAGLTCRLIPA---TLYPGRVILSLDFILFCLRLMHIFTISKT 919

Query: 204   LGPKIIMLQRMTSIEMXXXXXXIPTLRFFEFVVLIQSISGTSSHHEVMLSDRCVLLPVPL 263
             LGPKII+++RM            +  + FF F++ +   +S
Sbjct: 920   LGPKIIIVKRM----------MKDVFFFLFLLAVWVVS------------------- 947

Query: 264   CGVDGGLCVARQGILRQNEQRWRWIFRSVIYEPYLAMFGQVPSDVDGTTYDFAHCTFTGN 323
                       VA+Q IL  NE+R  W+FR  +Y  YL +FGQ+P  +DG  ++  HC+  G
Sbjct: 948   ------FGVAKQAILIHNERRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGT 1001

Query: 324   ES-KPLCVELD-EHNLPRFPEWITIPLVCIYMLSTNILLVNLLVAMF 368
             +  KP C E D     P FPEW+T+ L+C+Y+L TNILL+NLL+AMF
Sbjct: 1002  DPYKPKCPESDATQQRPAFPEWLTVLLLCLYLLFTNILLLNLLIAMF 1048


 Score = 48.0 bits (112), Expect = 3e-04
 Identities = 20/45 (44%), Positives = 30/45 (66%)

Query: 475   YTVGTVQENNDQVWKFQRYFLVQEYCSRLNIPFPFIVFAYFYMVV 519
             YT   VQE+ DQ+WKFQR+ L++EY R   P PFI+ ++ + +
Sbjct: 1050  YTFQQVQEHTDQIWKFQRHDLIEEYHGRPAAPPPFILLSHLQLFI 1094
```

FIGURE 4C

82

GCCAGCTTCTACGCTGCCTTCAGGACACAGACGTGCCCAATCATGGCTTCTTGGTGCTTGATTACAGCTCAAGTCTGGG
TCAAAATGAAGGGAGATGTGGTGGGCAGCCGCAGCCCTCAGCAACACAAGCGGAGCACAGGAACACCTCAGGGTCTTCC
AGTTCCCATCTCAGAAGGCTCAATGAAATCCTTCCTTCCTGTCCACACCATCGTGCTTATCAGGGAGAATGTGTGCAAG
TGTGGCTATGCCCAGAGCCAGCACATGGAAGGCACCCAGATCAACCAAAGTGAGAAATGGAACTACAAGAAACACACCA
AGGAATTTCCTACCGACGCCTTTGGGGATATTCAGTTTGAGACACTGGGGAAGAAAGGGAAGTATATACGTCTGTCCTG
CGACACGGACGCGGAAATCCTTTACGAGCTGCTGACCCAGCACTGGCACCTGAAAACACCCAACCTGGTCATTTCTGTG
ACCGGGGCGCCAAGAACTTCGCCCTGAAGCCGCGCATGCGCAAGATCTTCAGCCGGCTCATCTACATCGCGCAGTCCA
AAUGTGCTTGGATTCTCACGGGAGGCACCCATTATGGCCTGATGAAGTACATCGGGGAGGTGGTGAGAGATAACACCAT
CAGCAGGAGTTCAGAGGAGAATATTGTGGCCATTGGCATAGCAGCTTGGGGCATGGTCTCCAACCGGGACACCCTCATC
AGGAATTGCGATGCTGAGGGCTATTTTTTAGCCCAGTACCTTATGGATGACTTCACAAGAGATCCACTGTATATCCTGG
ACAACAACCACACACATTTGCTGCTCGTGGACAATGGCTGTCATGGACATCCCACTGTCGAAGCAAAGCTCCGGAATCA
GCTAGAGAAGTATATCTCTGAGCGCACTATTCAAGATTCCAACTATGGTGGCAAGATCCCCATTGTGTGTTTTGCCCAA
CGAGGTGGAAAAGAGACTTTGAAAGCCATCAATACCTCCATCAAAAATAAAATTCCTTGTGTGGTGGTGGAAGGCTCGG
GCCAGATCGCTGATGTGATCGCTAGCCTGGTGGAGGTGGAGGATGCCCTGACATCTTCTGCCGTCAAGGAGAAGCTGGT
GCGCTTTTTACCCCGCACGGTGTCCCGGCTGCCTGAGGAGGAGACTGAGAGTTGGATCAAATGGCTCAAAGAAATTCTC
GAATGTTCTCACCTATTAACAGTTATTAAAATGGAAGAAGCTGGGGATGAAATTGTGAGCAATGCCATCTCCTACGCTC
TATACAAAGCCTTCAGCACCAGTGAGCAAGACAAGGATAACTGGAATGGGCAGCTGAAGCTTCTGCTGGAGTGGAACCA
CCTGGACTTAGCCAATGATGAGATTTTCACCAATGACCGCCGATGGGAGAAGAGCAAACCGAGGCTCAGAGACACAATA
ATCCAGGTCACATGGCTGGAAAATGGTAGAATCAAGGTTGAGAGCAAAGATGTGACTGACGGCAAAGCCTCTTCTCATA
TGCTGGTGGTTCTCAAGTCTGCTGACCTTCAAGAAGTCATGTTTACGGCTCTCATAAAGGACAGACCCAAGTTTGTCCG
CCTCTTTCTGGAGAATGGCTTGAACCTACGGAAGTTTCTCACCCATGATGTCCTCACTGAACTCTTCTCCAACCACTTC
AGCACGCTTGTGTACCGGAATCTGCAGATCGCCAAGAATTCCTATAATGATGCCCTCCTCACGTTTGTCTGGAAACTGG
TTGCCAACTTCCGAAGAGGCTTCCGGAAGGAAGACAGAAATGGCCGGGACGAGATGGACATAGAACTCCACGACGTGTC
TCCTATTACTCGGCACCCCCTGCAAGCTCTCTTCATCTGGGCCATTCTTCAGAATAAGAAGGAACTCTCCAAAGTCATT
TGGGAGCACACCAGGGGCTGCACTCTGGCAGCCCTGGGAGCCAGCAAGCTTCTGAAGACTCTGGCCAAAGTGAAGAACG
ACATCAATGCTGCTCGGGGAGTCCGAGGAGCTGGCTAATGAGTACGAGACCCGGGCTGTTGAGCTGTTCACTGAGTGTTA
CAGCAGCGATGAAGACTTGGCAGAACAGCTGCTGGTCTATTCCTGTGAAGCTTGGGGTGGAAGCAACTGTCTGGAGCTG
GCGGTGGAGGCCACAGACCAGCATTTCATCGCCCAGCCTGGGGTCCAG

FIGURE 5A

GAGGGGAGGGCTGTGCCCGTCCCATGCTTGCAAGGATGCTGACGATGCCCTTATCTCTGGGTCCAGGAAGAAACCTGTC
GACAAGCACAAGAAGCTGCTTTGGTACTATGTGGCGTTCTTCACCTCCCCCTTCGTGGTCTTCTCCTGGAATGTGGTCT
TCTACATCGCCTTCCTCCTGCTGTTTGCCTACGTGCTGCTCATGGATTTCCATTCGGTGCCACACCCCCCCGAGCTGGT
CCTGTACTCGCTGGTCTTTGTCCTCTTCTGTGTGATGAAGTGAGACAG

FIGURE 5B

84

ATGGAGCAGGGGGTGGCGCTCGTGGAGGAGGCTCGGGCAGCACAGGAGCCCACTGAGGGGGTGGGAGGCTCAGGCATGG
TGCGCTGCAGGTCCCGAGCCCTGCCCCACGGGAAGGCAGCTACGGCCCGCCCCGGTTCCCGCTCACGCCACTCCTTCCA
CACTTCCCTGCAAGCTGAGGGTGCCAGCTCTGGCCTTGGCCAGCCCAGAAAGGGGCTCCCACAGTGCAGCGGTGGGCTG
AAGGGCTCCTCAAGTGCCGCCAAAGTGGGAGCCCAGGCAGAGGAGGTGCCGAGAGCAAGCGAGGGCTGTGAGGACTGCC
AGCACGCTGTCACCTCTCAGAAGCGTAAGGGACTGGCTGATGTCTTATCACGGACTGGGAACAACTGGGACAGTGTCTG
CCCCACAAGTGGGTGGTACGTAAATGGGGTGAATTATTTTTACTGACCTGTGGAATGTGATGGACACGCTGGGGCTTTTT
TACTTCATAGCAGGAATTGTATTTCGGCTCCACTCTTCTAATAAAAGCTCTTTGTATTCTGGACGAGTCATTTTCTGTC
TGGACTACATTATTTTCACTCTAAGATTGATCCACATTTTTACTGTAAGCAGAAACTTAGGACCCAAGATTATAATGCT
GCAGAGGATGACGAGCATTGAGATGAGCTCATCTGGAAGCTCCATTCCAACACTGAGGTTCTTTGAGTTTGTGGTTTTA
ATTCAAAGCATTTCTGGGACATCCAGTCATCATGAAGTCATGCTATCTGATCGATGTGTTCTTCTTCCTGTTCCTCTTT
GCGGTGTGGATGGTGGCCTTTGCGTGGCCAGGCAAGGGATCCTTAGGCAGAATGAGCAGCGCTGGAGGTGGATATTCCG
TTCGGTCATCTACGAGCCCTACCTGGCCATGTTCGGCCAGGTGCCCAGTGACGTGGATGGTACCACGTATGACTTTGCC
CACTGCACCTTCACTGGGAATGAGTCCAAGCCACTGTGTGTGGAGCTGGATGAGCACAACCTGCCCCGGTTCCCCGAGT
GGATCACCATCCCCCCTGGTGTGCATCTACATGTTATCCACCAACATCCTGCTGGTCAACCTGCTGGTCGCCATGTTTGG
GTCTGTAGCCGCTGGCTAGTTCAGGTTCTTGACTTTGGGACAGAAAATAATTTGAAAGTGAGTCAAAAGCAAAAGCAA
GCAAGAGAGTTCACTGCAAAGCCAAAGTACACTCTAGCAGCCGCTGGTTTCAGGAGATGGACCTCAGCTGTCACTGCAT
GTCTCCAGCCAGCTAGGTGTTTGCCAGGGACAGGACGCCAAGGGCACAAGATATCGCTGGAGATGCACAAAGGGAAAAT
TGCAGAATTCTCTCAGGGACAACACCAGATGGCCACTGGTTGTCAAGGAGACTTTAAGAACCATCTCAGATGGGGCGGC
TACACGCTGCGCACCGTCCAGGAGAACAATGACCAGGTCTGGAAGTTCCAGAGGTACTTCCTGGTGCAGGAGTACTGCA
GCCGCCTCAATATCCCCTTCCCCTTCATCGTCTTCGCTTACTTCTACATGGTGGTGAAGAAGTGCTTCAAGTGTTGCTG
CAACGAGAAAAACATGGAGTCTTCTGTCTGCTCTGTGGAGGCAGGTGAAGATGCTTACAATTATAGGGAACATAAGGAA
CGCTCAAAAGAGCTTTTTGGGAGCCAGTGTGCCTTGATGCTAGTCTTTGCTGCCACTCTGATTCGTTGCCTGTTTTATT
TGGAGGGCATTGGAAATGCGTGA

FIGURE 5C

```
        1           11          21          31          41          51
        |           |           |           |           |           |
    1 MASWCLITAQ VWVKMKGDVV GSRSPQQHKR STGTPQGLPV PISEGSMKSF LPVHTIVLIR   60
   61 ENVCKCGYAQ SQHMEGTQIN QSEKWNYKKH TKEFPTDAFG DIQFETLGKK GKYIRLSCDT  120
  121 DALILYELLT QHWHLKTPNL VISVTGGAKN FALKPRMRKI FSRLIYIAQS KGAWILTGGT  180
  181 HYGLMKYIGE VVRDNTISRS SEENIVAIGI AAWGMVSNRD TLIRNCDAEG YFLAQYLMDD  240
  241 FTRDPLYILD NNHTHLLLVD NGCHGHPTVE AKLRNQLEKY ISERTIQDSN YGGKIPIVCF  300
  301 AQGGGKETLK AINTSIKNKI PCVVVEGSGQ IADVIASLVE VEDALTSSAV KEKLVRFLPR  360
  361 TVSRLPEEET ESWIKWLKEI LECSHLLTVI KMEEAGDEIV SNAISYALYK AFSTSEQDKD  420
  421 NWNGQLKLLL EWNQLDLAND EIFTNDRRWE SKPRLRDTI IQVTWLENGR IKVESKDVTD  480
  481 GKASSHMLVV LKSADLQEVM FTALIKDRPK FVRLFLENGL NLRKFLTHDV LTELFSNHFS  540
  541 TLVYRNLQIA KNSYNDALLT FVWKLVANFR RGPRKEDRNG RDEMDIELHD VSPITRHPLQ  600
  601 ALFIWAILQN KKELSKVIWE QTRGCTLAAL GASKLLKTLA KVKNDINAAG ESEELANEYE  660
  661 TRAVELFTEC YSSDEDLAEQ LLVYSCEAWG GSNCLELAVE ATDQHFIAQP GVQ
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FIGURE 6A

86

```
        1            11           21           31           41           51
        |            |            |            |            |            |
    1 RGGLCPSHAC KDADDALISG SRKKPVDKHK KLLWYYVAFF TSPFVVFSWN VVFYIAFLLL      60
   61 FAYVLLMDPH SVPHPPELVL YSLVFVLFCD EVRQ
```

FIGURE 6B

```
        1.          11          21          31          41          51
        |           |           |           |           |           |
  1  MEQGVALVEE ARAAQEPTEG VGGSGMVGCR SRALPHGKAA TARPGSRSRH SFHTSLQAEG   60
 61  ASSGLGQPRK GLPQCSGGLK GSSSAAKVGA QAEEVPRASE GCEDCQHAVT SQKRKGLADV  120
121  LSRTGNNWDS VCPTSGWYVN GVNYFTDLWN VMDTLGLFYF IAGIVFRLHS SNKSSLYSGR  180
181  VIFCLDYIIF TLRLIHIFTV SRNLGPKIIM LQRMTSIEMS SSGSSIPTLR FFEFVVLIQS  240
241  ISGTSSHHEV MLSDRCVLLP VPLCGVDGGL CVARQGILRQ NEQRWRWIFR SVIYEPYLAM  300
301  FGQVPSDVDG TTYDFAHCTF TGNESKPLCV ELDEHNLPRF PEWITIPLVC IYMLSTNILL  360
361  VNLLVAMFGC VAGGLVQVLD FGTENNLKVS QKQKQARELT AKPKYTLAAA GFRRWTSAVT  420
421  ACIQPARCLP GTGRQGHKIS LEMHKGKIAE FSQGQHQMAT GCQGDFKNHL RWGGYTVGTV  480
481  QENNDQVWKF QRYFLVQEYC SRLNIPFPFI VFAYFYMVVK KCFKCCCKEK NMESSVCSVE  540
541  AGRDAYNYRE HKEGSKELFG SQCAIMLVFA ATLIRCLFYL EGIGNA
```

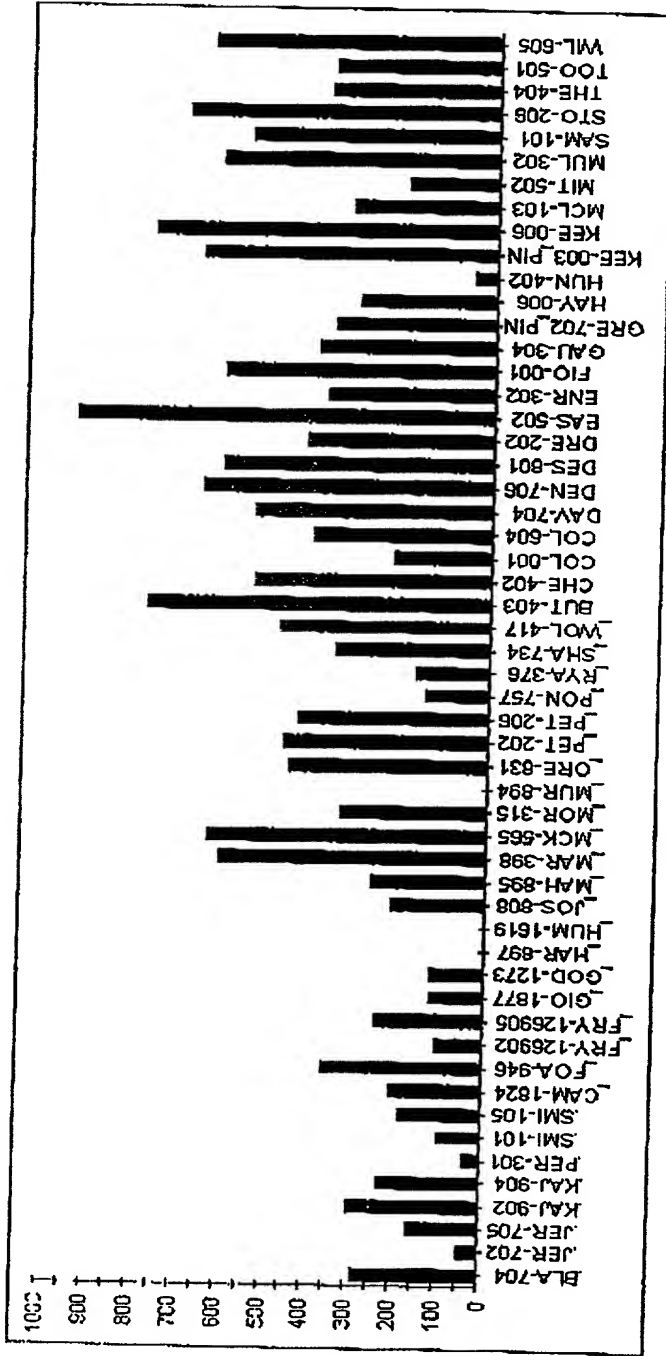# FIGURE 6C

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FIGURE 3A

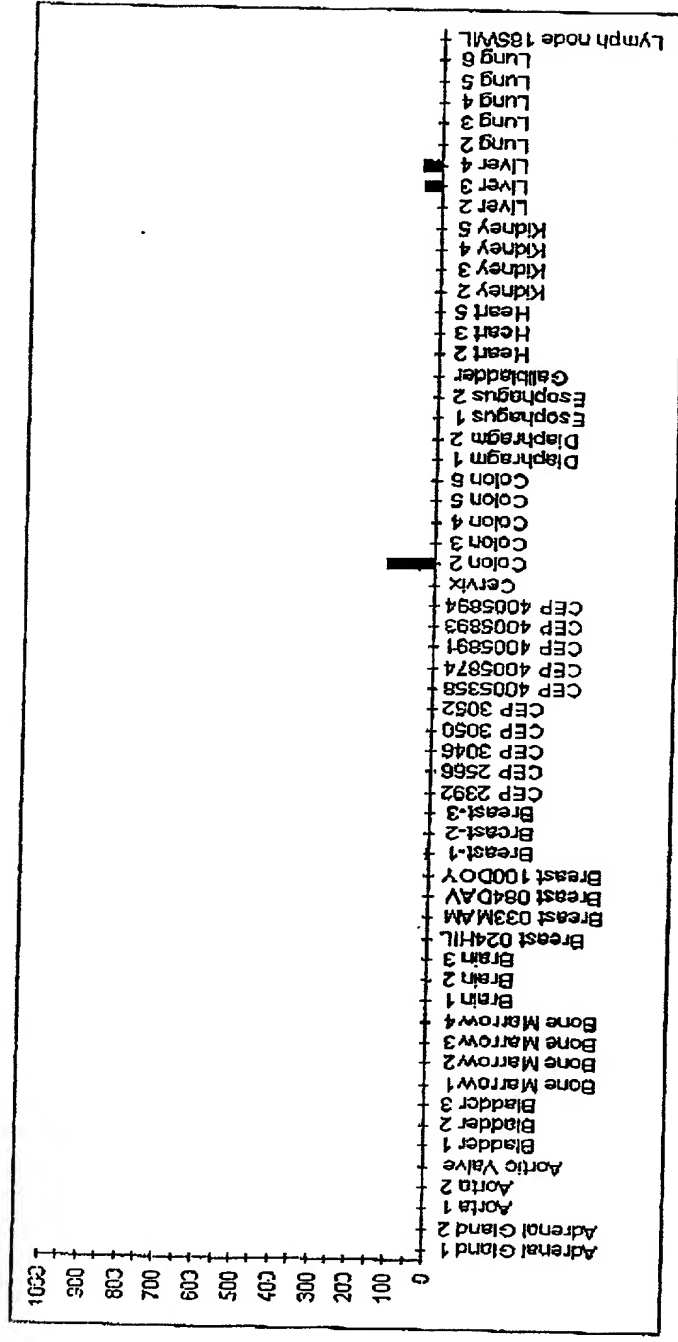**FIGURE 3B**

FIGURE 3C